

Attorney Docket No.: DEX-0259  
Inventors: Sun et al.  
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#### REMARKS

Claim 1-5, 7, 8, 15 and 18 are pending in the instant patent application. Claim 18 has been withdrawn from consideration by the Examiner as being drawn to a nonelected invention and subsequently canceled without prejudice by applicants. Claims 1-5, 7, 8 and 15 have been rejected. Claim 1 has been amended. Support for these amendments is provided in the specification at page 14, lines 1-9. Thus, no new matter is added by these amendments. Reconsideration is respectfully requested in light of these amendments and the following remarks.

#### I. Rejection of Claims 1-5, 7 and 8 under 35 U.S.C. 101 and 112, first paragraph

The rejection of claims 1-5, 7 and 8 under 35 U.S.C. 101 and 112, first paragraph for lack of utility have been maintained.

Applicants respectfully traverse this rejection.

The Courts and the MPEP are clear; to properly reject a claimed invention under 35 U.S.C. 101, the Office must (A) make a prima facie showing that the claimed invention lacks utility, and (B) provide a sufficient evidentiary basis for factual assumptions relied upon in establishing the prima facie showing. See MPEP 2107.02 and In re Gaubert, 524 F.2d 1222, 1224, 187 USPQ

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664, 666 (CCPA 1975). The Examiner in the instant rejection suggests that the data from the Gene Expression Analysis set forth in Example 1 of the instant application is "totally inconclusive, as other data bases or results published somewhere else may show that SEQ ID NO:84 is expressed in normal prostate tissue as well". However, the Examiner has failed to provide any evidence whatsoever to support this statement and has provided no showing that another database or publication showed a different result from SEQ ID NO:84 than disclosed herein. Thus, this rejection clearly fails to meet the required burden of the Examiner to establish a prima facie showing of lack of utility.

As also made clear in MPEP 2107.02, is that where Applicant has specifically asserted that an invention has a particular utility, that assertion cannot simply be dismissed by Office personnel as being "wrong" even when there may be reason to believe that that the assertion is not entirely accurate. Rather, Office personnel must determine if the assertion of utility is believable to a person of ordinary skill in the art based upon the totality of evidence and reasoning provided. An assertion is credible unless (A) the logic underlying the assertion is seriously flawed, or (B) the facts upon which the assertion is based are inconsistent with the logic underlying the

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assertion.

In the instant application, Applicants have disclosed SEQ ID NO:84 to be a CLASP2 marker, meaning expressed only in prostate cancer tissue. Contrary to the Examiner's suggestion, the source of SEQ ID NO:84 is clearly identified as tissues from patients with cancer. See page 116, lines 10-12. Further, contrary to the Examiner's suggestion, statistical analyses performed by the CLASP algorithm is taught at page 117, lines 4-15 and further at page 117, lines 23-27 it is taught that to qualify as a CLASP2 marker, a gene must exhibit detectable expression in tumor tissues and undetectable expression in tumor tissues and undetectable expression in libraries from normal individuals and libraries from normal tissue obtained from diseased patients. Thus, the conclusion that SEQ ID NO:84 is a diagnostic marker for prostate cancer is based upon a logical analysis of factual data and establishes a credible utility for the instant claimed invention.

Any further maintenance of this rejection, without some showing supported by evidence by the Examiner of any flaw in the logic upon which the utility described herein is based, is clearly improper.

Withdrawal of this rejection under 35 U.S.C. 101 and 112, first paragraph is therefore respectfully requested.

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**II. Rejection of Claims 1-5, 7, 8 and 15 under 35 U.S.C. 112,  
first paragraph - Written Description**

The rejection of claims 1-5, 7, 8 and 15 under 35 U.S.C. 112, first paragraph, for lack of written description has been maintained. Specifically, the Examiner suggests that Applicants have not described nucleic acids which hybridize to SEQ ID NO:84 under stringent conditions or which have at least 85% sequence identity to SEQ ID NO:84.

Accordingly, in an earnest effort to advance the prosecution of this case, Applicants have amended claim 1 to delete part (d) drawn to nucleic acids having at least 85% sequence identity.

However, with respect to part (c), contrary to the Examiner's suggestion, the specification does describe nucleic acids which hybridize under stringent conditions to SEQ ID NO:84.

SEQ ID NO:83 of the instant application is an example of a nucleic acid sequence meeting this claim limitation.

Further, the skilled artisan can routinely determine, using methodologies outlined in detail in the instant specification at page 14, line 9 through page 16, line 19, additional nucleic acid sequences which hybridize under the defined stringent conditions of claim 1.

Accordingly, Applicants were clearly in possession of a

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nucleic acid sequence meeting the limitation of part (c) of claim 1. Further, limitations of the stringent conditions in part (c) of claim 1 define structural features of the claimed nucleic acid sequences so that one of skill in the art can predictably identify the encompassed molecules as being identical to those now claimed.

Thus, the claims as amended meet the written description requirements of 35 U.S.C. § 112, first paragraph. See MPEP § 2163.02.

Withdrawal of this rejection under 35 U.S.C. 112, first paragraph is therefore respectfully requested.

**III. Rejection of Claims 1, 2, 4, 5, 7 and 8 under 35 U.S.C. § 102(a)**

Claims 1, 2, 4, 5, 7 and 8 have been rejected under 35 U.S.C. § 102(a) as being anticipated by a sequence with accession No. AK027241. The Examiner suggests that the sequence of accession no. AK027241 is 21.7% identical to SEQ ID NO:84, with bp 5 to 936 99.6% identical to bp 3259-4190 of SEQ ID NO:84. Thus, the Examiner suggests that the sequence with accession no. AK027241 will hybridize specifically to SEQ ID NO:84 in accordance with part (c) of claim 1. The Examiner concludes

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based on this the sequence of accession no. AK027241 and SEQ ID NO: 84 would be expected to hybridize. Further, the Examiner suggests that this human cDNA was cloned into a vector and must have been used in host cells.

Applicants respectfully traverse this rejection.

The specification at page 14, line 9 through page 16, line 19 provides adequate description of stringent hybridization conditions and methods to determine if 2 sequences would hybridize under stringent conditions.

Contrary to the Examiner's assertion, the sequence of accession no. AK027241 would not hybridize to SEQ ID NO: 84 under stringent conditions. Page 14, line 26 to line 28 states that stringent hybridization is performed at about 25°C below the thermal melting point ( $T_m$ ) for the specific DNA hybrid under a particular set of conditions. The conditions are clearly set forth in section (c) of Claim 1. At page 14, line 30  $T_m$  is defined as "the temperature at which 50% of the target sequence hybridizes to a perfectly matched probe". The sequence of accession no. AK027241 is 2119 bp and SEQ ID NO: 84 is 4270 bp, therefore the greatest hybrid between the two sequences is 2119 bp. The alignment provided by the examiner indicates there is 928 bp identity between the 2 sequences. Therefore, there is

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56.2% mismatch between the 2 sequences  $[(1-(928/2119))*100]$ .

Page 15, line 10 states that the  $T_m$  decreases by 1-1.5°C for each 1% of mismatch between two nucleic acid sequences. Therefore, the  $T_m$  for the sequence provided in accession no. AK027241 and SEQ ID NO: 84 would be decreased by 56.2°C to 84.3°C.

Additionally, as described above stringent hybridization is performed about 25°C below  $T_m$ .

Therefore, the reduction in  $T_m$  due to the great percentage of mismatch, coupled with stringent hybridization being performed at about 25°C below the thermal melting point ( $T_m$ ) is sufficient to place the conditions for hybridization between the sequence of accession no. AK027241 and SEQ ID NO: 84 outside the stringent hybridization conditions set forth in claim 1.

Thus, the sequence disclosed in accession no. AK027241 does not teach a sequence meeting the elements of claim 1 section (c) and cannot anticipate the instant claimed invention.

Withdrawal of this rejection under 35 U.S.C. § 102(a) is therefore respectfully requested.

IV. Rejection of Claims 1, 2, 4, 5, 7 and 8 under 35 U.S.C. § 102(b)

Claims 1, 2, 4, 5, 7 and 8 have been rejected under 35 U.S.C. § 102(b) as being anticipated by a accession No.

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AF0123851. The Examiner suggests that accession No. AF0123851 discloses a sequence which shares 6.1% identity with SEQ ID NO:84 with bp 1 to 261 having 99.6% identity to bp 3695-3955 of SEQ ID NO:84. Additionally, the examiner states that the sequence of accession No. AF0123851 meets the limitation of being "substantially similar to at least 300 bp of SEQ ID NO: 84" because "substantially similar" is defined as having "nucleotide sequence identity in at least about 50%, more preferably 60% of the nucleotide bases, usually at least about 70%, more usually at least about 80%, preferably at least about 90%, and more preferably at least about 95-98% of the nucleotide bases."

Thus, the Examiner suggests that the sequence with accession no. AF0123851 will hybridize specifically to SEQ ID NO:84 as set forth in part (c) of claim 1. The Examiner concludes based on this that sequence of accession no. AF0123851 and SEQ ID NO: 84 would be expected to hybridize. Further, the Examiner suggests that this human cDNA was cloned into a vector and that host cells were made.

Applicants have amended Claim 1 section (c) to indicate that a nucleic acid must exhibit "at least 90% substantial sequence similarity to at least 300 nucleotides of the nucleic acid molecule of (a) or (b)". The nucleic acid of accession no.



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AF0123851 does not exhibit at least 90% substantial sequence similarity to at least 300 nucleotides of the nucleic acid molecule of (a) or (b).

Thus, the sequence disclosed in accession no. AK027241 does not teach a sequence meeting the elements of claim 1 section (c) as amended and cannot anticipate the instant claimed invention.

Withdrawal of this rejection under 35 U.S.C. § 102(a) is therefore respectfully requested.

**V. Rejection of Claim 15 under 35 U.S.C. § 102(b)**

The Examiner has maintained the rejection of claim 15 under 35 U.S.C. 102(b) as being anticipated by Gibco BRL Catalog. Arguments presented by Applicants in the last response were not found convincing as the Examiner suggests that the Gibco Catalog teaches "a means for determining any nucleic acid molecules, since they teach a kit comprising random primers".

Applicants respectfully traverse this rejection.

MPEP 2121.01 is clear; the disclosure in an asserted anticipating reference must provide an enabling disclosure of the desired subject matter. The desired subject matter in this case is a kit for detecting a risk of cancer or presence of cancer in a patient which comprising a means for detecting a specifically defined nucleic acid molecule. An enabling disclosure, in

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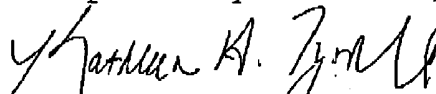
accordance with MPEP 2121.01 is a disclosure which places the public in possession of the invention before the date of the invention. In no way is the Gibco Catalog enabling for this kit for detection of a novel nucleic acid shown for the first time in the instant application to be indicative of the risk of or presence of cancer.

Withdrawal of this rejection under 35 U.S.C. 102(b) is therefore respectfully requested.

#### VI. Conclusion

Applicants believe that the foregoing comprises a full and complete response to the Office Action of record. Accordingly, favorable reconsideration and subsequent allowance of the pending claims is earnestly solicited.

Respectfully submitted,



Kathleen A. Tyrrell  
Reg. No. 38,350

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LICATA & TYRRELL P.C.  
66 E. Main Street  
Marlton, New Jersey 08053

(856) 810-1515